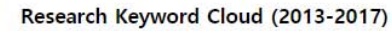




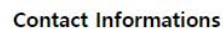
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Teaching

~~Teaching materials for Experiment in microbiology and biochemical engineering laboratory Course~~

2019 netbiolab experiment teaching material

2019 netbiolab experiment teaching material

Teaching materials for Yonsei Bioinformatics Course

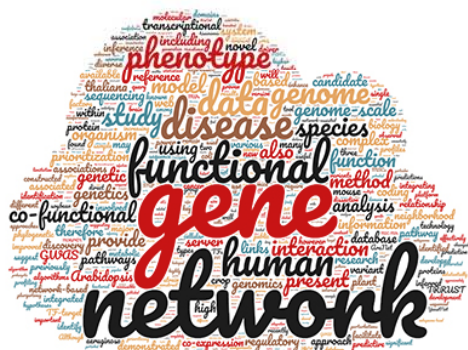
2018 Bioinformatics Kallisto Practice 2018 Bioinformatics WebMeV Practice 2018 Bioinformatics Machine Learning Practice 

Teaching materials for BIML workshop

BIML2017 practice 2 PPT file & python scripts

BIML2016 practice 1 PPT file

BIML2016 practice 2 python scripts



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1. www.cytoscape.org



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Cytoscape

Network Data Integration, Analysis, and Visualization in a Box

[Introduction](#) [Download 3.7.1](#)

Cytoscape is an [open source](#) software platform for visualizing complex networks and integrating these with any type of attribute data. A lot of [Apps](#) are available for various kinds of problem domains, including bioinformatics, social network analysis, and semantic web. [Learn more...](#)

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 **for Windows (64 bit)**

Java 8 will be automatically installed if not already present

Java 9 is not yet supported

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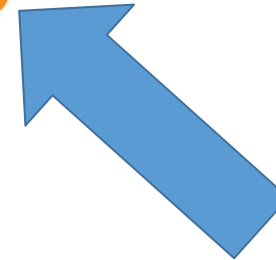
This is a tax deductible donation to a 501(c)(3) nonprofit organization,
The Cytoscape Consortium, Tax ID: 20-4909878.

License Agreement

Cytoscape is available as a platform-independent open-source Java application, released under the terms of the LGPL. By downloading Cytoscape, you agree that you have read the license agreement that follows and agree to its terms. If you don't agree, do not download Cytoscape.

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Window 32bit
MAC OS



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Download 3.7.1

Platform Specific Installers

Java 8 is required and is automatically installed for Windows and Mac OS

[Mac OS X](#)[Windows 64bit](#)[Linux](#)[Windows 32bit](#)

This is the **last version** of Cytoscape for Windows 32bit. Please consider upgrading your system to a 64 bit processor and using a 64 bit Java VM so you can take advantage of substantial improvements in Cytoscape speed and memory usage that enable faster processing and larger networks.

Archive Distributions

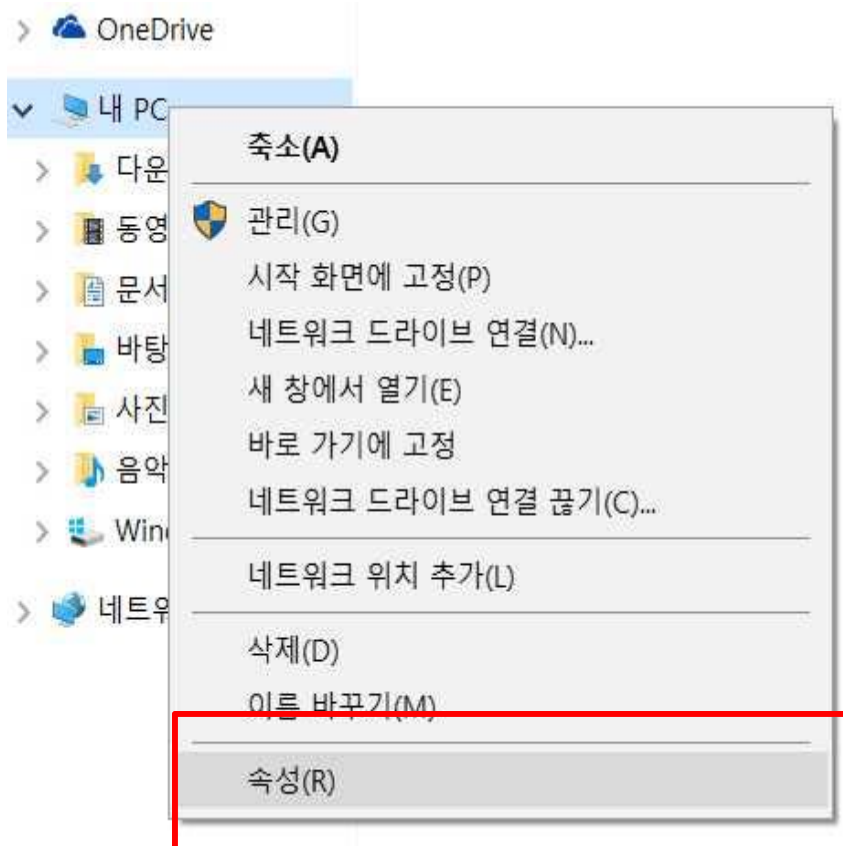
[Zip Archive](#)

for Windows

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for Mac/Unix

How to check your computer's OS version. (windows case)



컴퓨터에 대한 기본 정보 보기

Windows 버전

Windows 10 Home

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시스템

프로세서: Intel(R) Pentium(R) CPU N3540 @ 2.16GHz 2.16 GHz

설치된 메모리(RAM): 4.00GB(3.88GB 사용 가능)

시스템 종류: 64비트 운영 체제, x64 기반 프로세서

펜 및 터치: 이 디스플레이에 사용할 수 있는 펜 또는 터치식 입력이 없습니다.

컴퓨터 이름, 도메인 및 작업 그룹 설정

컴퓨터 이름: 200laptop

전체 컴퓨터 이름: 200laptop

컴퓨터 설명:

작업 그룹: WORKGROUP

Windows 정품 인증

Windows 정품 인증을 받았습니다. [Microsoft 소프트웨어 사용 조건 읽기](#)

제품 ID: 00326-10000-00000-AA758

Download java from

<http://java.sun.com/javase/downloads/index.jsp>

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Java Platform (JDK) 12

Java Platform, Standard Edition

Java SE 12

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Java SE 8u201 / Java SE 8u202 includes important bug fixes. Oracle strongly recommends that all Java SE 8 users upgrade to this release.
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JRE
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- [Java ME](#)
- [Java Card](#)
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- [Java Mission Control](#)

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Download Java 8 that suits your OS.

Oracle Technology Network / Java / Java SE / Downloads

Java SE Runtime Environment 8 Downloads

Do you want to run Java™ programs, or do you want to develop Java programs? If you want to run Java programs, but not develop them, download the Java Runtime Environment, or JRE™. The JDK includes the JRE, so you do not have to download both separately.

JRE 8u201 Checksum
JRE 8u202 Checksum

Java SE Runtime Environment 8u201

You must accept the Oracle Binary Code License Agreement for Java SE to download this software.

☒ Accept License Agreement ☐ Decline License Agreement

Product / File Description	File Size	Download
Linux x86	68.1 MB	jre-8u201-linux-i586.rpm
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Linux x64	64.91 MB	jre-8u201-linux-x64.rpm
Linux x64	80.73 MB	jre-8u201-linux-x64.tar.gz
Mac OS X x64	76.18 MB	jre-8u201-macosx-x64.dmg
Mac OS X x64	67.77 MB	jre-8u201-macosx-x64.tar.gz
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Java SE Runtime Environment 8u202

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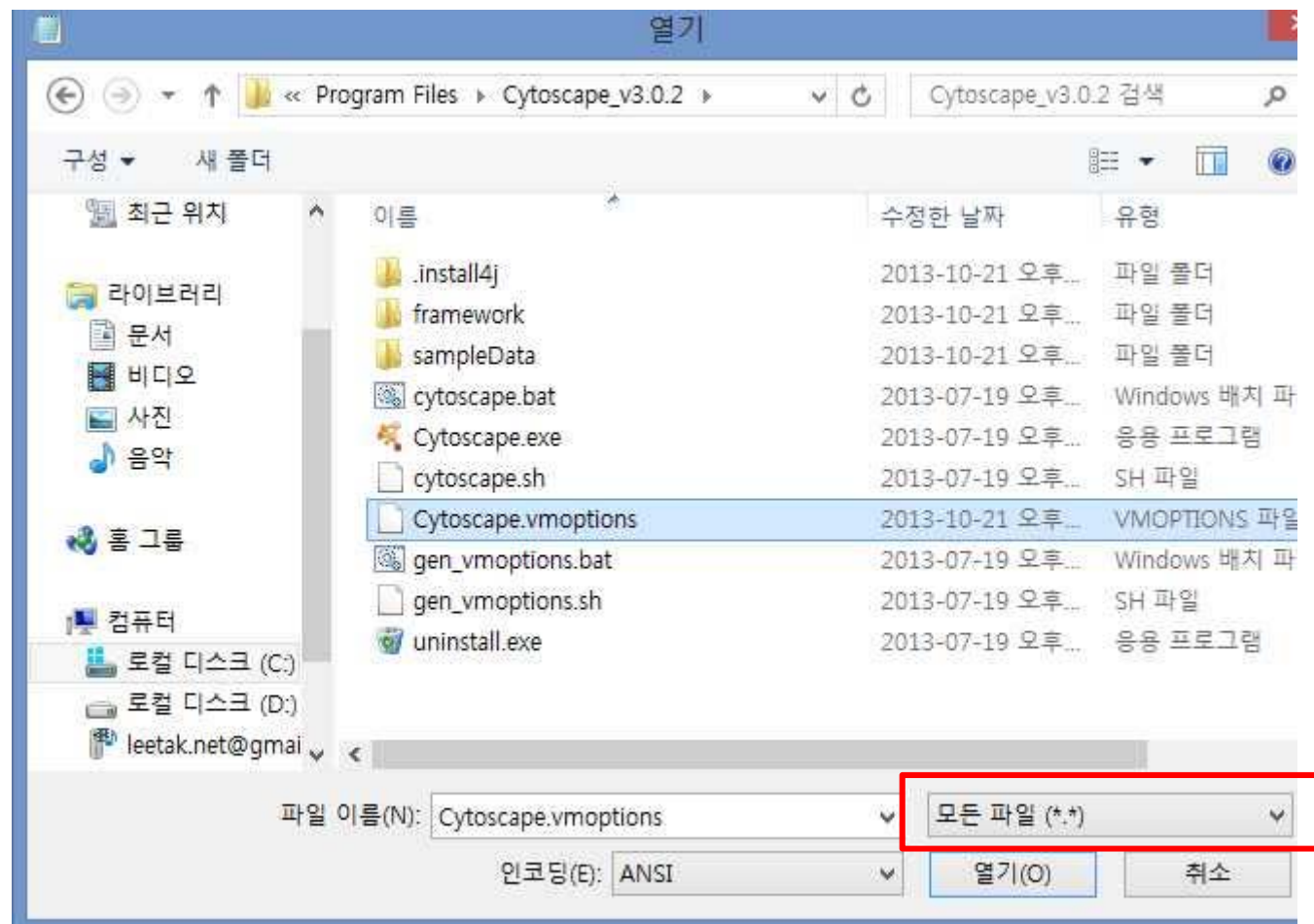
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Windows x86	68.4 MB	jre-8u202-windows-i586.tar.gz
Windows x64	73.7 MB	jre-8u202-windows-x64.exe
Windows x64	73.25 MB	jre-8u202-windows-x64.tar.gz

Install Java and Cytoscape by default setting.

Trouble shooting Java crashes

Run Notepad as “Administrator”

File → Open → cytoscape file → Open the file: Cytoscape_vmoptions



Trouble shooting Java crashes

Run Notepad as “Administrator”

File → Open → cytoscape file → Open the file: Cytoscape_vmoptions

Convert **-Xmx1250m** into **-Xmx512m** and save

LAB 6 :

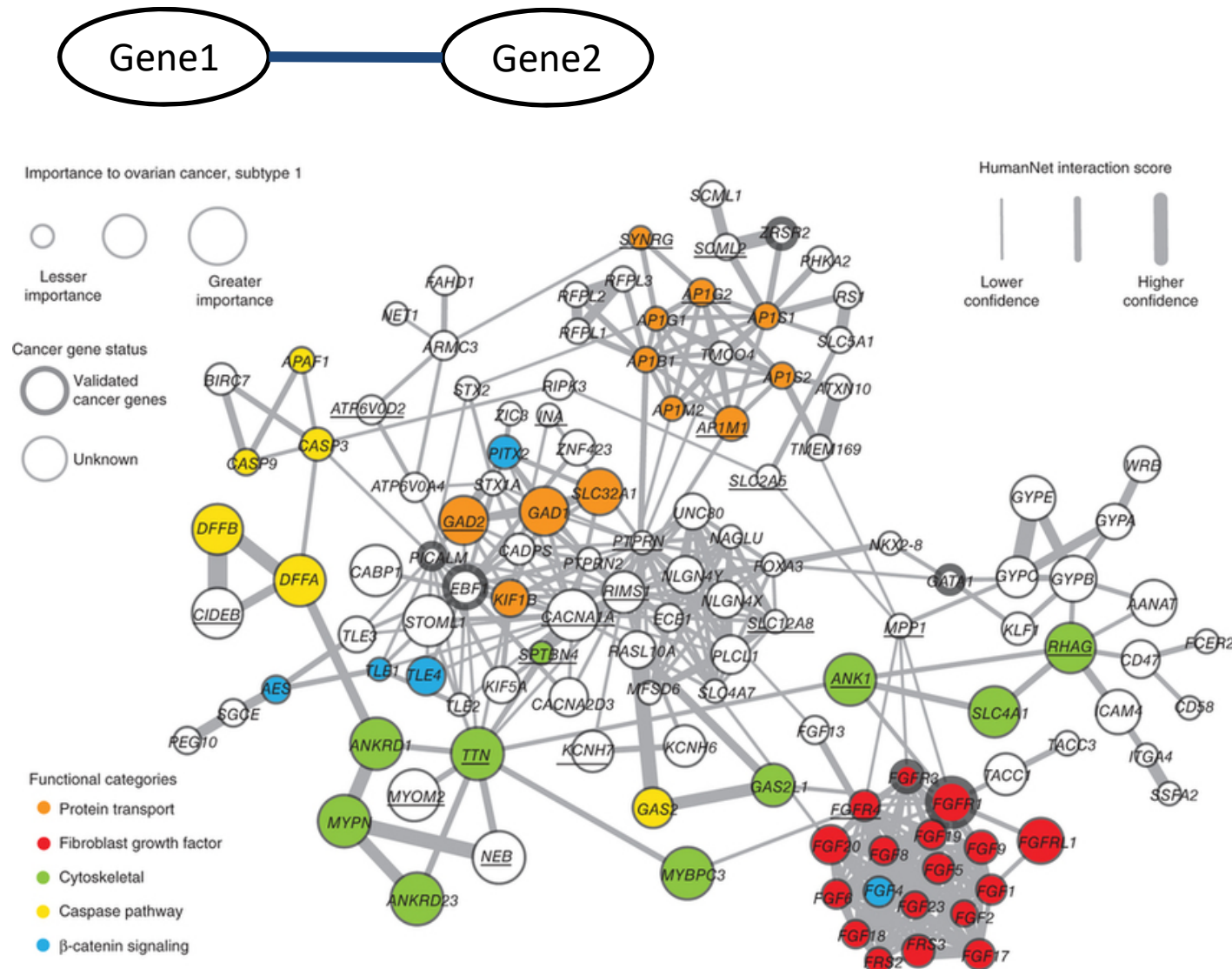
Visualization and analysis of functional gene networks using Cytoscape



1. Network : HumanNet v.1

a probabilistic functional gene network of 18,714 validated encoding genes of *Homo sapiens*. (Insuk *et al*, 2011)

We used subset of the network: 'breast cancer related genes'

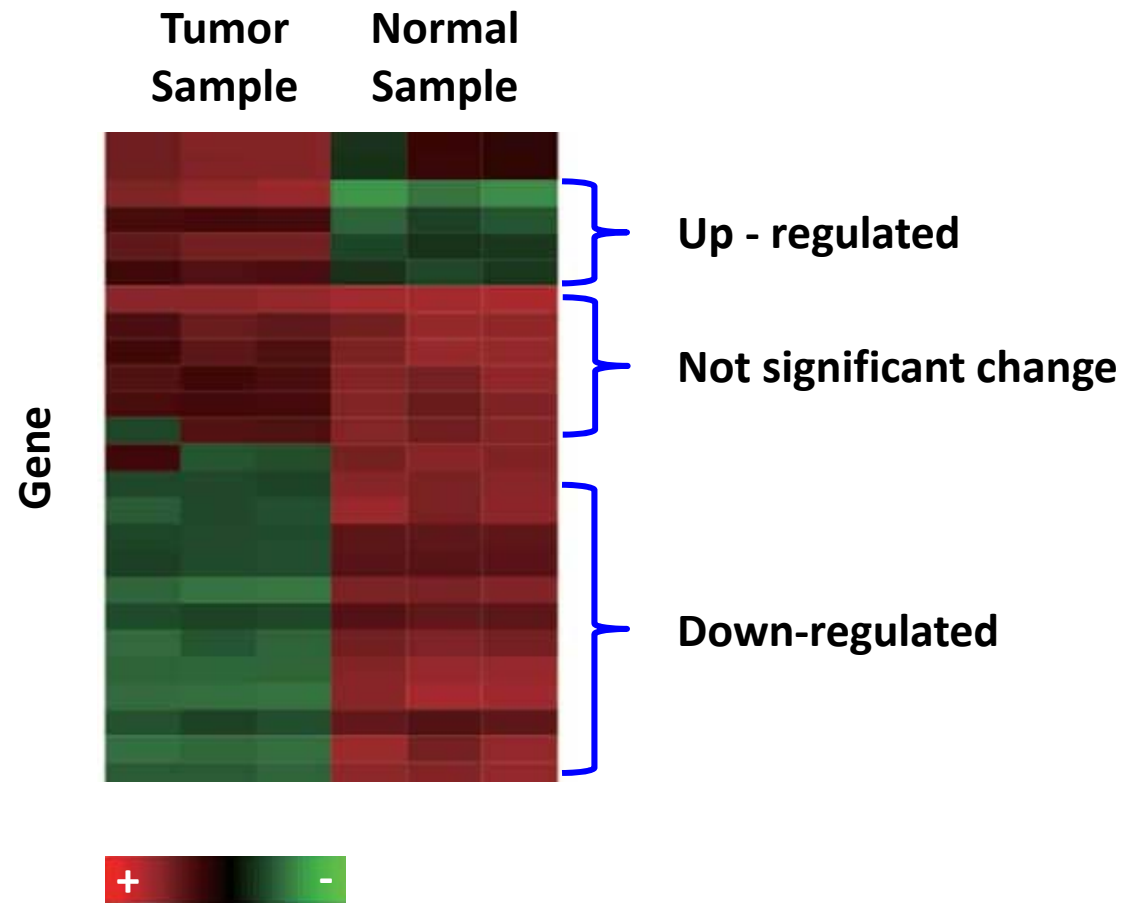
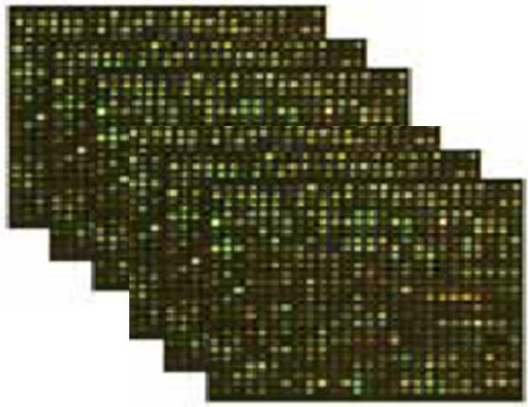


2. Expression data: RNA-seq data

Samples are from 3 Breast cancer patients and 3 normal .

Breast cancer patients have specific type of cancer : **Triple Negative Breast Cancer**

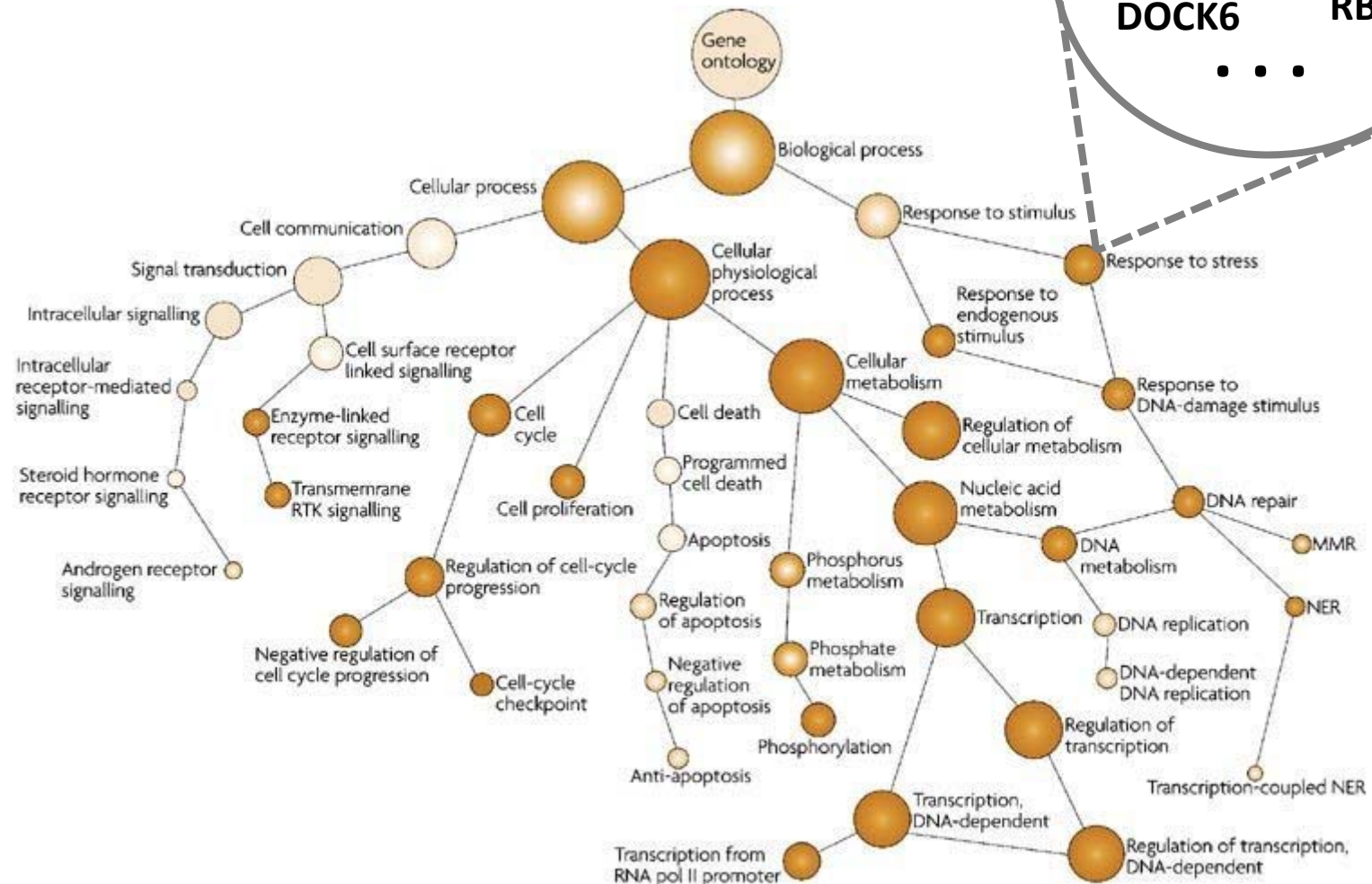
Data downloaded from : Gene Expression Omnibus (GEO) → A whole collection of various expression data

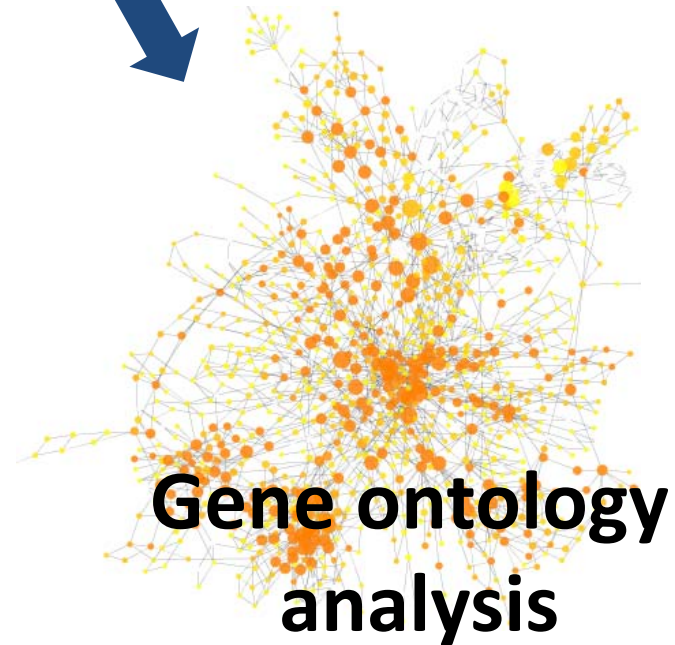
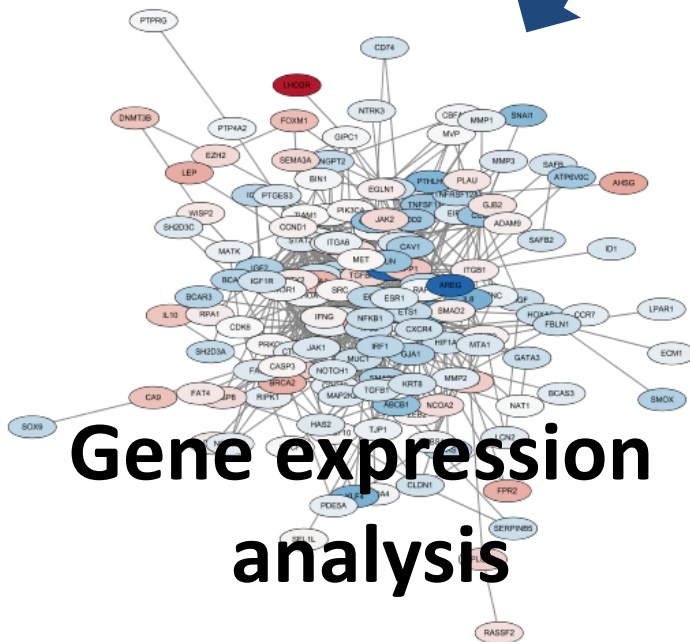
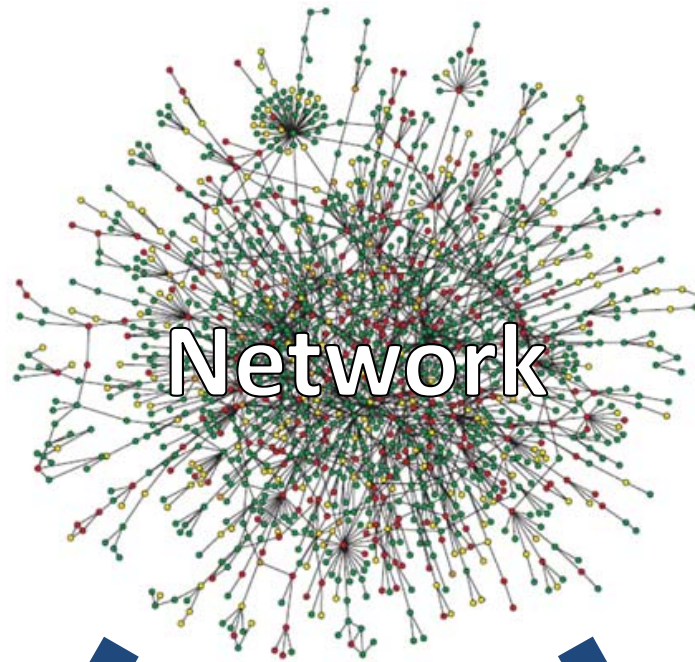


3. Gene Ontology : Gene-Function annotation data

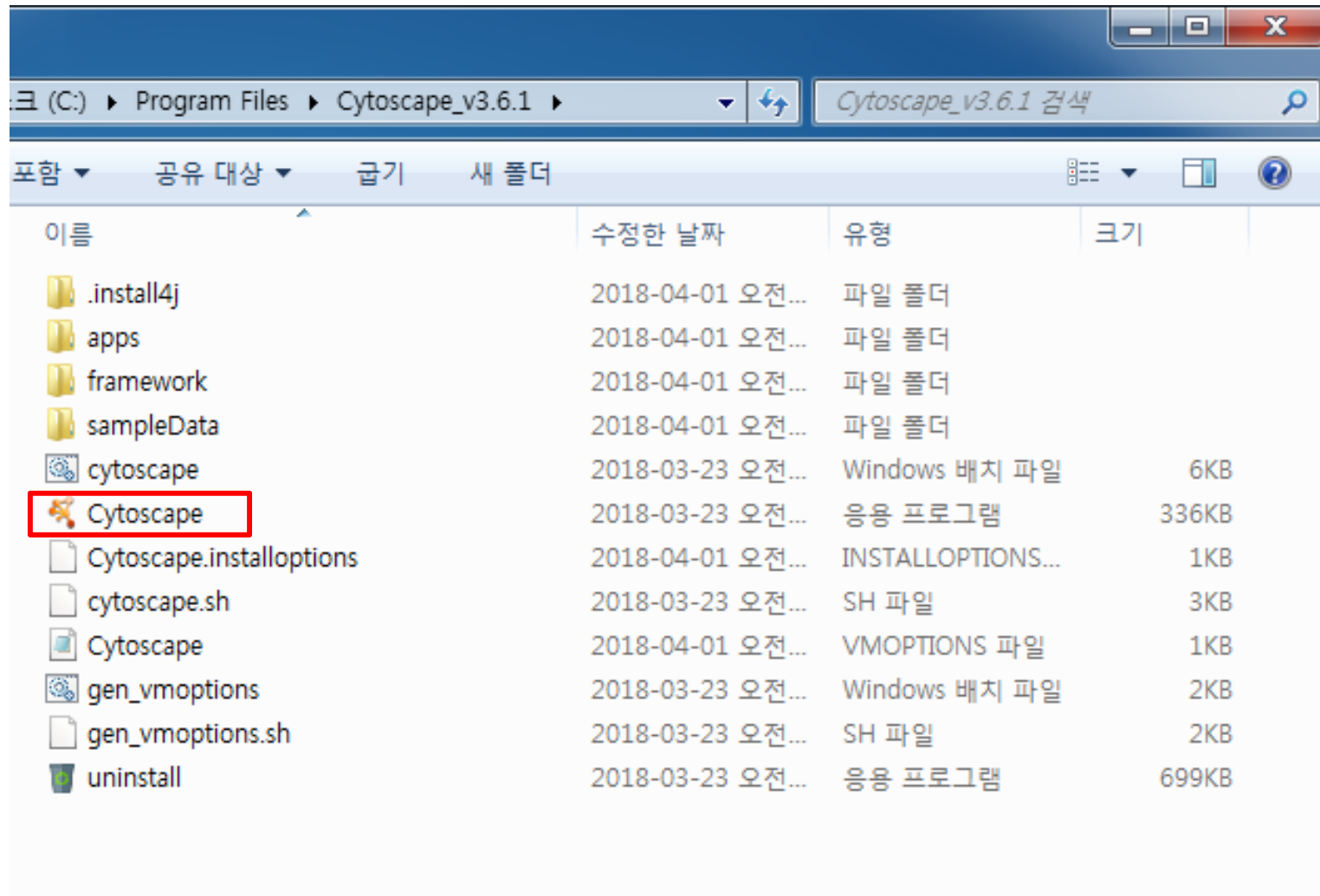
Described in 3 domains

- Molecular Function
- Cellular Component
- **Biological Process**

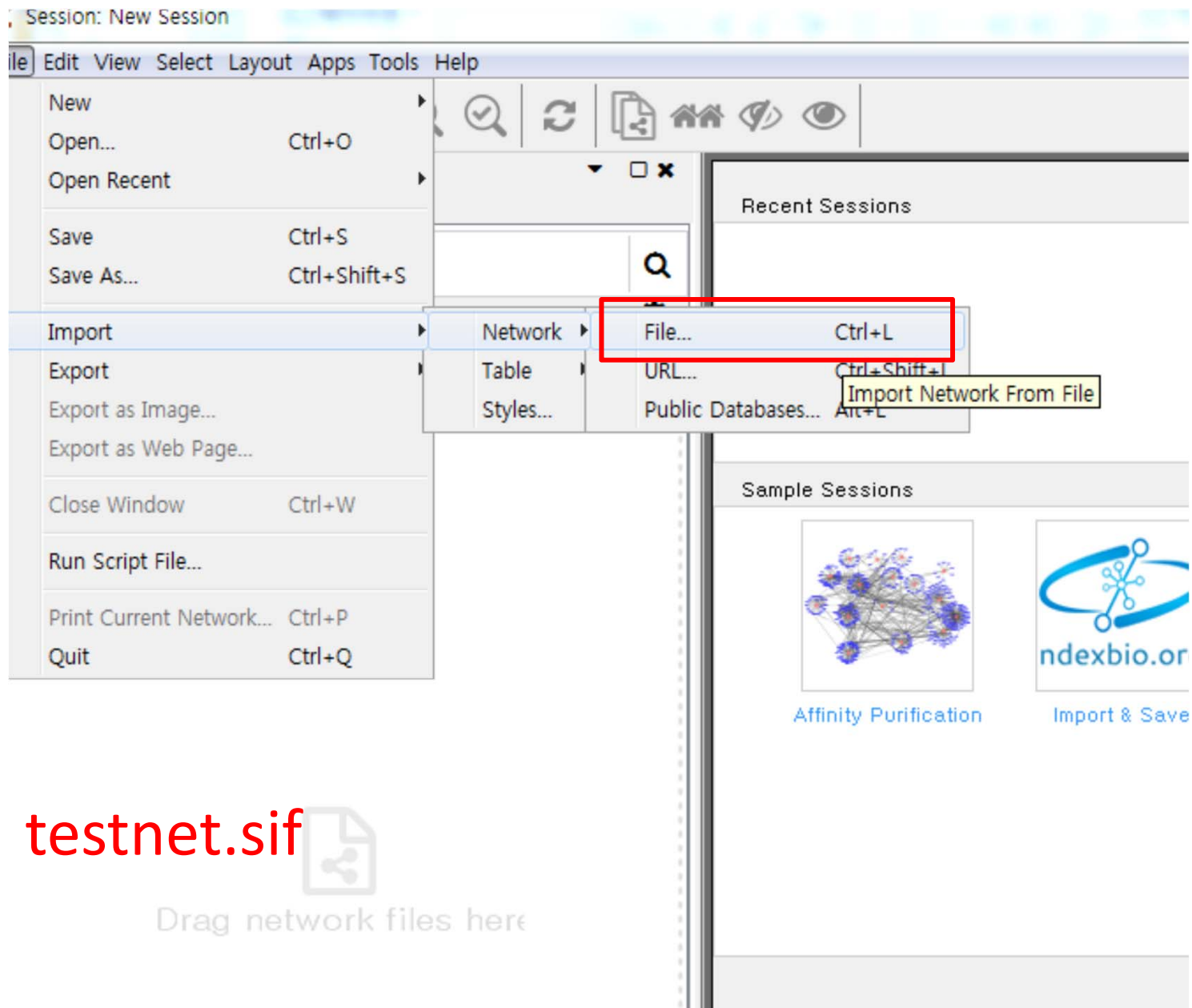




Running Cytoscape



Import network



Import expression data

DO_breastcancer.pvals

The screenshot displays the 'Easy Document Creator' application window. The main workspace shows a complex network diagram with numerous nodes (represented by blue squares) and edges (lines connecting the nodes). The nodes are labeled with gene symbols, including SOX9, CA9, AHSG, TNFRSF12A, LPAR1, FBLN1, and many others. A search bar at the top right of the workspace contains the text 'Enter search term...'. On the left side, a menu is open, showing options like 'File', 'Edit', 'View', 'Select', 'Layout', 'Apps', 'Tools', and 'Help'. The 'Import' option is highlighted, and a submenu is visible with options: 'Network', 'Table', 'Styles...', 'File...', 'Import Table From File', and 'Public Databases...'. The 'File...' option is further highlighted. Below the menu, there are various settings for the network diagram, such as 'Label', 'Label Color', 'Label Font Size' (set to 12), 'Shape', 'Size', 'Transparency' (set to 255), and 'Width' (set to 75.0). At the bottom, there is a 'Table Panel' with a table showing 'shared name' and 'name' for several genes. The 'Node Table' tab is selected.

shared name	name
SOX9	SOX9
CA9	CA9
AHSG	AHSG
TNFRSF12A	TNFRSF12A
LPAR1	LPAR1
FBLN1	FBLN1

Maximum color

Session: New Session

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select

default

Properties

Def. Map. Byp.

Border Paint

2.0 Border Width

Fill Color

Column LOG2FOLDexp

Mapping Type Continuous Mapping

Current Mapping

35.0 Height

Image/Chart 1

Label

Label Color

12 Label Font Size

Shape

Size

255 Transparency

Node Edge Network

Continuous Mapping Editor for Node Fill Color

Min=-16.4719403

LOG2FOLDexp

Max=16.4719403

Edit Handle Positions and Values

Handle Position: -4

Set Min and Max...

Add

Delete

Node Fill Color:

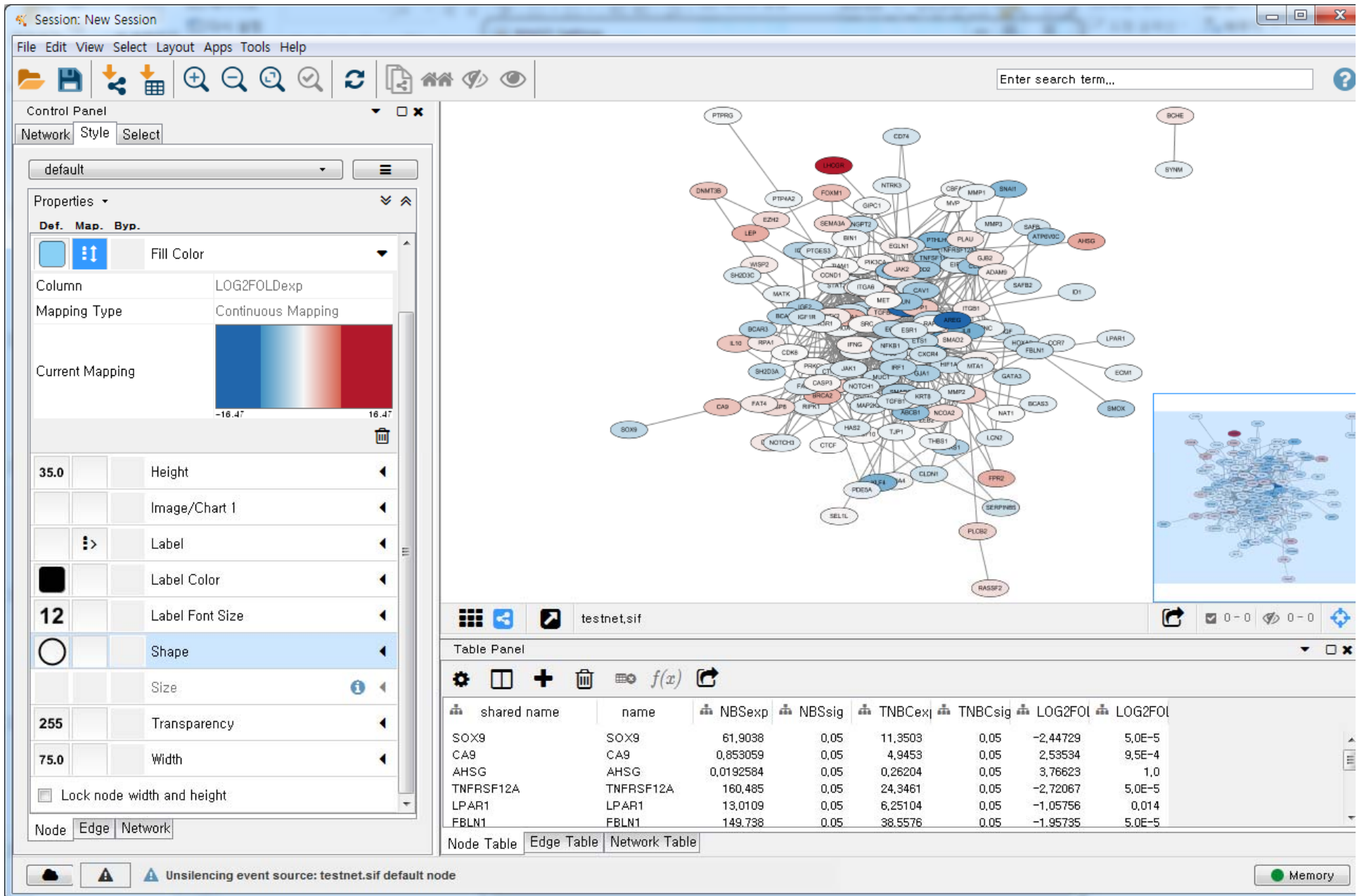
OK

Cancel

Node	Edge	Network
SOX		
CA9	CA9	0.853059 0.05 4.9453 0.05 2.53534 9.5E-4
AHSG	AHSG	0.0192584 0.05 0.26204 0.05 3.76623 1.0
TNFRSF12A	TNFRSF12A	160.485 0.05 24.3461 0.05 -2.72067 5.0E-5
LPAR1	LPAR1	13.0109 0.05 6.25104 0.05 -1.05756 0.014
FBLN1	FBLN1	149.738 0.05 38.5576 0.05 -1.95735 5.0E-5

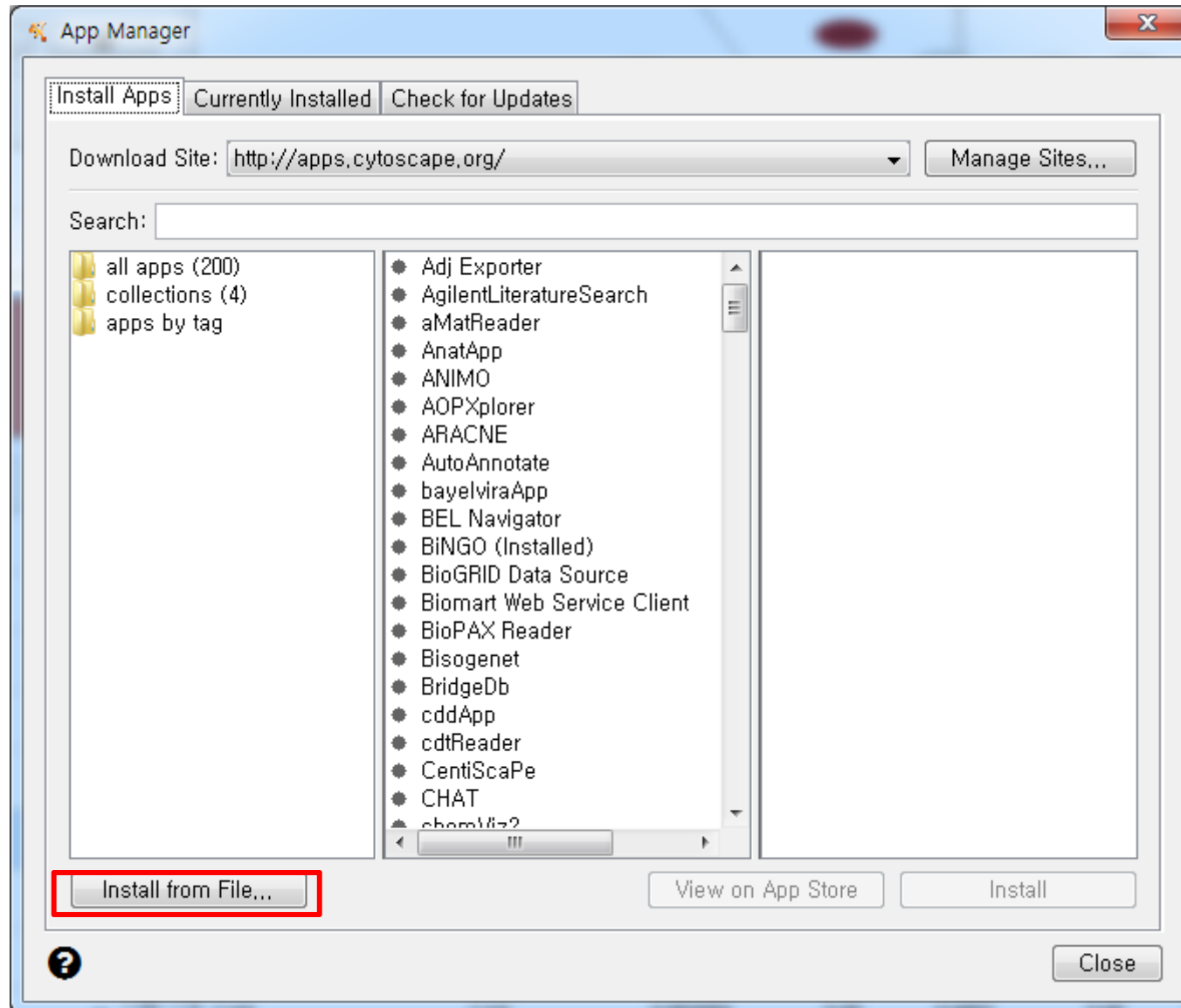
Node Table Edge Table Network Table

Memory



Installing BINGO

1. Apps → App manager → Install from File → BINGO.jar



Running BINGO

The screenshot shows the 'BINGO Settings' dialog box. Red arrows point from the following instructions to the corresponding fields in the dialog:

- Arrow 1 points to the 'Cluster name:' text box.
- Arrow 2 points to the 'Get Cluster from Network' checkbox.
- Arrow 3 points to the 'Select ontology file:' dropdown menu.
- Arrow 4 points to the 'Select namespace:' dropdown menu.
- Arrow 5 points to the 'Select organism/annotation:' dropdown menu.

The dialog box contains the following settings:

- BINGO settings**
- Buttons: Save settings as default, Help
- Cluster name: (empty text box)
- ☒ Get Cluster from Network ☐ Paste Genes from Text
- Do you want to assess over- or underrepresentation:
☒ Overrepresentation ☐ Underrepresentation
☒ Visualization ☐ No Visualization
- Select a statistical test: Hypergeometric test
- Select a multiple testing correction: Benjamini & Hochberg False Discovery Rate (FDR) correction
- Choose a significance level: 0.05
- Select the categories to be visualized: Overrepresented categories after correction
- Select reference set: Custom...
- Select ontology file: GO_Biological_Process
- Select namespace: biological_process
- Select organism/annotation: Saccharomyces cerevisiae
- Discard the following evidence codes: (empty text box)
- ☐ Check box for saving Data Save BINGO Data file i...
- Start BINGO

1) Select all genes in the network (Ctrl + A)

2) Apps → BINGO

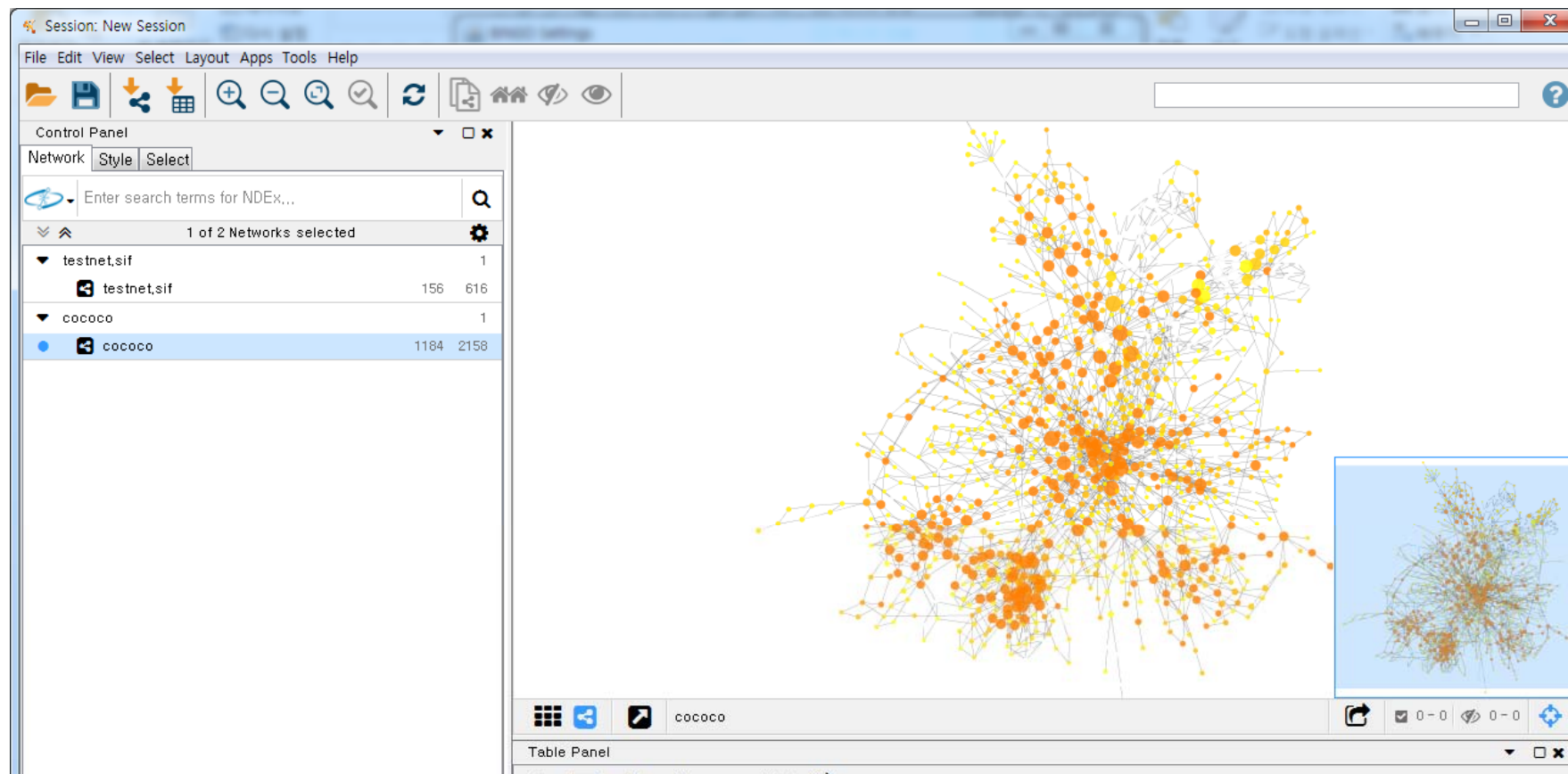
3) BiNGO settings

Type cluster name : any names

Select ontology file : →
custom : " file gene_ontology_ext.obo"

Select namespace → ---

Select organism/annotation →
custom " file : GOBP.BiNGO.txt"



BINGO output

cococo

GO: Homo sapiens. Biological Process. unknown. unknown

GO-ID	Description	p-val	corr p-val	cluster freq	total freq	genes
48522	positive regulation of cellular process	1.3329E-30	3.3190E-27	95/143	66.4%	2140/9792 ... ITGB1 CDKN1A ECM1 PTEN BRCA1 CTCF BRCA2 FOXM1 ETS1 TNF I...
48518	positive regulation of biological process	1.6067E-27	2.0004E-24	97/143	67.8%	2439/9792 ... ETS1 TNF IGF1R GJA1 CCND1 CHEK2 TNFSF10 AKT1 TNFSF11 SOX9...
42221	response to chemical	1.1041E-26	9.1640E-24	84/143	58.7%	1831/9792 ... BCAR3 ITGB1 CDKN1A PTEN BRCA1 ETS1 TNF IGF1R CASP8 CCND1...
70887	cellular response to chemical stimulus	6.1062E-25	3.8011E-22	70/143	48.9%	1313/9792 ... CDKN1A PTEN BRCA1 TNF IGF1R CASP3 AKT1 TNFSF11 CA9 SOX9 ...
10033	response to organic substance	4.0282E-24	2.0060E-21	66/143	46.1%	1194/9792 ... CDKN1A PTEN BRCA1 TNF IGF1R CASP8 CASP3 AKT1 TNFSF11 SOX...
48583	regulation of response to stimulus	1.8223E-23	7.5624E-21	78/143	54.5%	1742/9792 ... ITGB1 CDKN1A ECM1 PTEN BRCA1 FOXM1 TNF IGF1R GJA1 CASP8 ...
48584	positive regulation of response to stimulus	5.2031E-23	1.7482E-20	56/143	39.1%	876/9792 8... ECM1 PTEN BRCA1 FOXM1 TNF GJA1 CASP8 TNFSF10 TNFSF11 CC...
71310	cellular response to organic substance	5.9655E-23	1.7482E-20	60/143	41.9%	1021/9792 ... CDKN1A PTEN BRCA1 TNF IGF1R CASP3 AKT1 TNFSF11 SOX9 RAC1...
71363	cellular response to growth factor stimulus	6.3188E-23	1.7482E-20	41/143	28.6%	429/9792 4... CDKN1A NOTCH1 SRC PTEN PIK3R1 PRKCZ EGFR ERBB3 CASP3 ER...
9611	response to wounding	8.6795E-23	2.1612E-20	47/143	32.8%	597/9792 6... ITGB1 SRC TNC CXCR4 FPR2 PIK3R1 GATA3 TNF PRKCZ THBS1 CD...
70848	response to growth factor	1.0775E-22	2.4390E-20	41/143	28.6%	435/9792 4... CDKN1A NOTCH1 SRC PTEN PIK3R1 PRKCZ EGFR ERBB3 CASP3 ER...
9719	response to endogenous stimulus	1.5612E-22	3.2395E-20	46/143	32.1%	576/9792 5... CDKN1A SRC PTEN PIK3R1 GATA3 BRCA1 TNF PRKCZ THBS1 EGFR ...
31325	positive regulation of cellular metabolic process	1.7359E-22	3.3248E-20	68/143	47.5%	1358/9792 ... CDKN1A PTEN BRCA1 CTCF BRCA2 FOXM1 ETS1 TNF IGF1R CASP8...
50896	response to stimulus	3.6028E-22	6.1286E-20	114/143	79.0%	3949/9792 ... TNC ETS1 TNF IGF1R CCND1 PLAU CHEK2 TNFSF10 AKT1 TNFSF11 ...
1902531	regulation of intracellular signal transduction	3.6920E-22	6.1286E-20	52/143	36.3%	775/9792 7... ECM1 PTEN FOXM1 TNF IGF1R GJA1 CASP8 TNFSF10 TNFSF11 RAC...
9967	positive regulation of signal transduction	4.6197E-22	7.1894E-20	45/143	31.4%	562/9792 5... ECM1 SRC FPR1 LPAR1 CXCR4 GATA3 TNF PRKCZ THBS1 EGFR G1...

Select All Unselect All

Select nodes

Report

Assignment : Draw given Network with Cytoscape on your own.

Things to include

1. Date of the experiment and the day (Mon, Tue, Wed, Thur, Fri)
2. Results with “figures of your own” (**1 network file with gradient color, 1 with BINGO output**)
3. Discussion
4. References

Discussion should include :

- What the network visualization tells you.
(What information does the network give you? What can you tell from the expression data and function enrichment analysis using Bingo?
→ No correct answer for this. Just write what you think)
- Other type of visualization may give you additional points. If you have made modifications, describe what you have done in the report

Data to draw the network can be found in : www.netbiolab.org → teaching

Find Cytoscape at : www.cytoscape.org

Report

Lab Address: Science Research Center (과학원) S323 Questions:

Monday, Tuesday Thursday class: 조재원 (dreadcupper@naver.com)

Wednesday, Friday class: 이성호 (shlee354@gmail.com)

Due date : Experiment date → Due date

Monday class (4/8) → 4/15 (18:00)

Tuesday class (4/2) → 4/9 (18:00)

Wednesday class(4/3) → 4/10 (18:00)

Thursday class (4/4) → 4/11 (18:00)

Friday class (4/5) → 4/12 (18:00)